MiR-125a-3p timely inhibits oligodendroglial maturation and is pathologically up-regulated in human multiple sclerosis

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Supplementary Table S1. List of all Gene Ontology biological processes enriched in miR-125a-3p targets.

GO_id	Term	N of genes	p-value (fdr)
GO:0009987	cellular process	820	5.25E-31
GO:0044763	single-organism cellular process	706	5.6E-31
GO:0065007	biological regulation	664	4,00E-25
GO:0008150	biological_process	847	9.16E-25
GO:0044699	single-organism process	731	2.07E-24
GO:0050789	regulation of biological process	638	3.82E-24
GO:0050794	regulation of cellular process	601	5.22E-21
GO:0008152	metabolic process	590	6.29E-15
GO:0048731	system development	307	3.54E-14
GO:0007399	nervous system development	185	1.51E-13
GO:0044237	cellular metabolic process	510	2.96E-13
GO:0007275	multicellular organismal development	336	7.08E-13
GO:0051716	cellular response to stimulus	359	1.65E-12
GO:0044767	single-organism developmental process	369	3.43E-12
GO:0071704	organic substance metabolic process	527	4.87E-12
GO:0044700	single organism signaling	294	8.09E-12
GO:0032502	developmental process	368	8.45E-12
GO:0048519	negative regulation of biological process	321	1.32E-11
GO:0007154	cell communication	301	1.37E-11
GO:0044238	primary metabolic process	510	2.93E-11
GO:0048518	positive regulation of biological process	368	3.13E-11

GO:0019222	regulation of metabolic process	416	3.23E-11
GO:0048523	negative regulation of cellular process	300	3.49E-11
GO:0016043	cellular component organization	318	8.12E-11
GO:0048513	organ development	238	9.98E-11
GO:0043170	macromolecule metabolic process	441	1.15E-10
GO:0048856	anatomical structure development	330	1.69E-10
GO:0044707	single-multicellular organism process	380	2.08E-10
GO:0010646	regulation of cell communication	218	2.55E-10
GO:0048522	positive regulation of cellular process	325	2.81E-10
GO:0071840	cellular component organization or biogenesis	324	3.18E-10
GO:0044260	cellular macromolecule metabolic process	408	3.93E-10
GO:0048583	regulation of response to stimulus	238	5.37E-10
GO:0007165	signal transduction	271	6,00E-10
GO:0050896	response to stimulus	407	6,00E-10
GO:0051179	localization	309	7.13E-10
GO:0032501	multicellular organismal process	386	9.91E-10
GO:0023051	regulation of signaling	206	1.38E-9
GO:0051128	regulation of cellular component organization	184	1.67E-9
GO:0022008	neurogenesis	132	2.26E-9
GO:0009966	regulation of signal transduction	184	5.94E-9
GO:0031323	regulation of cellular metabolic process	361	1.14E-8
GO:0048699	generation of neurons	123	1.14E-8
GO:0006464	cellular protein modification process	197	2.1E-8
GO:0043412	macromolecule modification	205	2.24E-8
GO:0032879	regulation of localization	182	2.61E-8
GO:0030154	cell differentiation	250	4.17E-8
GO:0044267	cellular protein metabolic process	233	4.17E-8
GO:0080090	regulation of primary metabolic process	348	4.69E-8
GO:0019538	protein metabolic process	267	4.83E-8
GO:0007166	cell surface receptor signaling pathway	135	7.6E-8
GO:0035556	intracellular signal transduction	123	8.61E-8
GO:0043067	regulation of programmed cell death	122	8.77E-8
GO:0000904	cell morphogenesis involved in differentiation	62	9.35E-8
GO:0010941	regulation of cell death	127	1.24E-7
GO:0065008	regulation of biological quality	209	1.69E-7
GO:0060255	regulation of macromolecule metabolic process	344	1.7E-7
GO:1902578	single-organism localization	209	1.82E-7
GO:0048869	cellular developmental process	257	3.03E-7
GO:0044765	single-organism transport	195	3.91E-7
GO:0051234	establishment of localization	243	4.94E-7
GO:0042981	regulation of apoptotic process	118	5.21E-7
GO:0030182	neuron differentiation	88	5.21E-7
GO:0006810	transport	235	5.74E-7
GO:0009653	anatomical structure morphogenesis	174	1,00E-06
GO:0006996	organelle organization	201	1.01E-6
GO:0009968	negative regulation of signal transduction	93	1.22E-6

GO:0023057	negative regulation of signaling	101	1.62E-6
GO:0048468	cell development	135	1.78E-6
GO:0044710	single-organism metabolic process	257	1.78E-6
GO:0010648	negative regulation of cell communication	101	2.27E-6
GO:0009893	positive regulation of metabolic process	245	2.56E-6
GO:0065009	regulation of molecular function	189	2.8E-6
GO:0012501	programmed cell death	89	3.25E-6
GO:0031175	neuron projection development	59	3.74E-6
GO:0006793	phosphorus metabolic process	143	3.78E-6
GO:0007417	central nervous system development	85	3.8E-6
GO:0051049	regulation of transport	136	4.01E-6
GO:0006915	apoptotic process	87	4.01E-6
GO:0048666	neuron development	71	5.06E-6
GO:2000811	negative regulation of anoikis	9	5.33E-6
GO:0048667	cell morphogenesis involved in neuron differentiation	44	6.06E-6
GO:0008219	cell death	90	6.89E-6
GO:0016265	death	90	6.89E-6
GO:0051246	regulation of protein metabolic process	183	7.42E-6
GO:0048812	neuron projection morphogenesis	46	8.35E-6
GO:0048585	negative regulation of response to stimulus	108	9.01E-6
GO:0016310	phosphorylation	95	1.05E-5
GO:0009892	negative regulation of metabolic process	182	1.26E-5
GO:0051239	regulation of multicellular organismal process	183	1.52E-5
GO:0051640	organelle localization	43	1.52E-5
GO:0007409	axonogenesis	38	1.52E-5
GO:0010604	positive regulation of macromolecule metabolic process	195	1.57E-5
GO:1902531	regulation of intracellular signal transduction	110	1.67E-5
GO:0043069	negative regulation of programmed cell death	78	1.71E-5
GO:0006796	phosphate-containing compound metabolic process	137	1.79E-5
GO:0031325	positive regulation of cellular metabolic process	204	2.3E-5
GO:0010647	positive regulation of cell communication	123	2.48E-5
GO:0051641	cellular localization	143	2.63E-5
GO:0032268	regulation of cellular protein metabolic process	169	2.66E-5
GO:0006468	protein phosphorylation	78	2.86E-5
GO:0061564	axon development	39	3.64E-5
GO:0060548	negative regulation of cell death	81	3.79E-5
GO:0023056	positive regulation of signaling	114	4.14E-5
GO:0050790	regulation of catalytic activity	153	4.32E-5
GO:0042127	regulation of cell proliferation	116	5.49E-5
GO:0007420	brain development	68	5.84E-5
GO:0060322	head development	71	5.85E-5
GO:2000209	regulation of anoikis	9	5.92E-5
GO:0031399	regulation of protein modification process	123	6.31E-5
GO:0043933	macromolecular complex subunit organization	137	8.15E-5
GO:0033554	cellular response to stress	115	9,00E-05
GO:0060341	regulation of cellular localization	97	1.02E-4

GO:0071702	organic substance transport	127	1.02E-4
GO:0043066	negative regulation of apoptotic process	74	1.11E-4
GO:0010001	glial cell differentiation	24	1.12E-4
GO:0010605	negative regulation of macromolecule metabolic process	162	1.29E-4
GO:0009888	tissue development	133	1.29E-4
GO:0048584	positive regulation of response to stimulus	133	1.53E-4
GO:0051656	establishment of organelle localization	34	1.56E-4
GO:0031401	positive regulation of protein modification process	84	1.63E-4
GO:0045595	regulation of cell differentiation	122	1.69E-4
GO:0006950	response to stress	195	1.69E-4
GO:0044093	positive regulation of molecular function	119	1.69E-4
GO:0001775	cell activation	54	1.86E-4
GO:0051270	regulation of cellular component movement	66	1.94E-4
GO:0071822	protein complex subunit organization	95	1.94E-4
GO:0040011	locomotion	88	1.94E-4
GO:0009967	positive regulation of signal transduction	101	1.94E-4
GO:0051130	positive regulation of cellular component organization	97	1.95E-4
GO:0060284	regulation of cell development	74	1.95E-4
GO:0032989	cellular component morphogenesis	82	2.08E-4
GO:0006928	movement of cell or subcellular component	93	2.08E-4
GO:0031324	negative regulation of cellular metabolic process	161	2.14E-4
GO:0044723	single-organism carbohydrate metabolic process	52	2.36E-4
GO:0042063	gliogenesis	27	2.46E-4
GO:0010033	response to organic substance	153	2.76E-4
GO:0051247	positive regulation of protein metabolic process	106	2.8E-4
GO:0051726	regulation of cell cycle	77	2.84E-4
GO:0050793	regulation of developmental process	161	2.86E-4
GO:0044802	single-organism membrane organization	54	2.95E-4
GO:0016192	vesicle-mediated transport	84	3.09E-4
GO:0008284	positive regulation of cell proliferation	71	3.16E-4
GO:0044249	cellular biosynthetic process	252	3.16E-4
GO:0032270	positive regulation of cellular protein metabolic process	99	3.74E-4
GO:0001934	positive regulation of protein phosphorylation	70	4.38E-4
GO:0034645	cellular macromolecule biosynthetic process	208	4.38E-4
GO:0051050	positive regulation of transport	75	4.51E-4
GO:0007264	small GTPase mediated signal transduction	38	4.64E-4
GO:0000902	cell morphogenesis	74	4.65E-4
GO:1901576	organic substance biosynthetic process	255	4.86E-4
GO:0010721	negative regulation of cell development	34	5,00E-04
GO:0022610	biological adhesion	81	5.02E-4
GO:0042327	positive regulation of phosphorylation	72	5.18E-4
GO:0070828	heterochromatin organization	7	5.29E-4
GO:0007167	enzyme linked receptor protein signaling pathway	53	5.33E-4
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	39	5.48E-4
GO:0016477	cell migration	65	5.65E-4
GO:0006355	regulation of transcription, DNA-templated	205	5.7E-4

GO:0009059	macromolecule biosynthetic process	208	6.34E-4
GO:0009058	biosynthetic process	259	6.57E-4
GO:0050767	regulation of neurogenesis	60	6.77E-4
GO:0007155	cell adhesion	80	6.8E-4
GO:0009889	regulation of biosynthetic process	241	7.13E-4
GO:0009894	regulation of catabolic process	65	7.78E-4
GO:0046907	intracellular transport	88	8.24E-4
GO:1903506	regulation of nucleic acid-templated transcription	204	8.68E-4
GO:0001944	vasculature development	51	8.72E-4
GO:0005975	carbohydrate metabolic process	56	8.96E-4
GO:0022607	cellular component assembly	123	9.15E-4
GO:0019438	aromatic compound biosynthetic process	176	9.36E-4
GO:0040012	regulation of locomotion	63	9.36E-4
GO:0031326	regulation of cellular biosynthetic process	237	9.8E-4
GO:0033043	regulation of organelle organization	89	9.83E-4
GO:2001141	regulation of RNA biosynthetic process	204	9.83E-4
GO:1901698	response to nitrogen compound	67	1.01E-3
GO:2000112	regulation of cellular macromolecule biosynthetic process	221	1.07E-3
GO:0042221	response to chemical	193	1.07E-3
GO:0018130	heterocycle biosynthetic process	175	1.07E-3
GO:0051649	establishment of localization in cell	110	1.15E-3
GO:2000145	regulation of cell motility	58	1.16E-3
GO:0030334	regulation of cell migration	56	1.16E-3
GO:0030030	cell projection organization	76	1.16E-3
GO:0045664	regulation of neuron differentiation	50	1.16E-3
GO:0061024	membrane organization	57	1.17E-3
GO:0050768	negative regulation of neurogenesis	28	1.17E-3
GO:0051674	localization of cell	69	1.21E-3
GO:1902533	positive regulation of intracellular signal transduction	70	1.21E-3
GO:0045321	leukocyte activation	44	1.23E-3
GO:0048870	cell motility	69	1.25E-3
GO:0010468	regulation of gene expression	238	1.28E-3
GO:0072358	cardiovascular system development	73	1.28E-3
GO:0072359	circulatory system development	73	1.28E-3
GO:0051302	regulation of cell division	31	1.3E-3
GO:0008366	axon ensheathment	16	1.3E-3
GO:0030900	forebrain development	41	1.3E-3
GO:0034654	nucleobase-containing compound biosynthetic process	170	1.3E-3
GO:0035295	tube development	61	1.31E-3
GO:0009719	response to endogenous stimulus	96	1.32E-3
GO:0051047	positive regulation of secretion	37	1.32E-3
GO:0043408	regulation of MAPK cascade	56	1.38E-3
GO:0051650	establishment of vesicle localization	22	1.42E-3
GO:0050853	B cell receptor signaling pathway	9	1.46E-3
GO:1902589	single-organism organelle organization	138	1.52E-3
GO:0051252	regulation of RNA metabolic process	208	1.53E-3

GO:0009056	catabolic process	108	1.55E-3
GO:0010556	regulation of macromolecule biosynthetic process	225	1.57E-3
GO:0045596	negative regulation of cell differentiation	60	1.67E-3
GO:1902580	single-organism cellular localization	61	1.67E-3
GO:0006351	transcription, DNA-templated	153	1.67E-3
GO:0032402	melanosome transport	7	1.87E-3
GO:0044248	cellular catabolic process	93	1.87E-3
GO:0022603	regulation of anatomical structure morphogenesis	75	2.08E-3
GO:0070085	glycosylation	28	2.12E-3
GO:0060429	epithelium development	86	2.17E-3
GO:0033036	macromolecule localization	132	2.22E-3
GO:0032774	RNA biosynthetic process	153	2.3E-3
GO:1903320	regulation of protein modification by small protein conjugation or removal	26	2.39E-3
GO:0016050	vesicle organization	24	2.4E-3
GO:0046777	protein autophosphorylation	25	2.51E-3
GO:0007010	cytoskeleton organization	70	2.52E-3
GO:0001568	blood vessel development	47	2.55E-3
GO:0001655	urogenital system development	36	2.55E-3
GO:0007265	Ras protein signal transduction	24	2.6E-3
GO:2001236	regulation of extrinsic apoptotic signaling pathway	23	2.68E-3
GO:0001932	regulation of protein phosphorylation	92	2.68E-3
GO:1901362	organic cyclic compound biosynthetic process	179	2.68E-3
GO:0032401	establishment of melanosome localization	7	2.68E-3
GO:0051904	pigment granule transport	7	2.68E-3
GO:0046579	positive regulation of Ras protein signal transduction	8	2.75E-3
GO:0051098	regulation of binding	30	2.75E-3
GO:0006486	protein glycosylation	27	2.75E-3
GO:0043413	macromolecule glycosylation	27	2.75E-3
GO:0031396	regulation of protein ubiquitination	24	2.75E-3
GO:0030097	hemopoiesis	54	2.76E-3
GO:0080134	regulation of response to stress	89	2.78E-3
GO:0010564	regulation of cell cycle process	45	2.78E-3
GO:0051171	regulation of nitrogen compound metabolic process	236	2.78E-3
GO:0032880	regulation of protein localization	73	2.79E-3
GO:0070372	regulation of ERK1 and ERK2 cascade	25	2.79E-3
GO:0051046	regulation of secretion	57	2.8E-3
GO:0018193	peptidyl-amino acid modification	59	2.97E-3
GO:0051960	regulation of nervous system development	64	2.97E-3
GO:0042552	myelination	15	3.03E-3
GO:0006357	regulation of transcription from RNA polymerase II promoter	126	3.03E-3
GO:0030335	positive regulation of cell migration	36	3.06E-3
GO:0043085	positive regulation of catalytic activity	95	3.1E-3
GO:0031344	regulation of cell projection organization	46	3.1E-3
GO:0051648	vesicle localization	22	3.1E-3
GO:0010243	response to organonitrogen compound	59	3.17E-3
GO:0001763	morphogenesis of a branching structure	26	3.29E-3

GO:1902532	negative regulation of intracellular signal transduction	40	3.29E-3
GO:0045665	negative regulation of neuron differentiation	22	3.39E-3
GO:0098609	cell-cell adhesion	50	3.42E-3
GO:0042592	homeostatic process	97	3.47E-3
GO:0070271	protein complex biogenesis	70	3.47E-3
GO:0006461	protein complex assembly	70	3.47E-3
GO:2000026	regulation of multicellular organismal development	120	3.52E-3
GO:0051905	establishment of pigment granule localization	7	3.56E-3
GO:0060562	epithelial tube morphogenesis	37	3.59E-3
GO:1901700	response to oxygen-containing compound	93	3.59E-3
GO:0042325	regulation of phosphorylation	97	3.64E-3
GO:0045893	positive regulation of transcription, DNA-templated	110	3.75E-3
GO:1903508	positive regulation of nucleic acid-templated transcription	110	3.75E-3
GO:0051272	positive regulation of cellular component movement	37	3.75E-3
GO:0007423	sensory organ development	52	3.75E-3
GO:0043410	positive regulation of MAPK cascade	40	3.75E-3
GO:1902582	single-organism intracellular transport	73	3.76E-3
GO:0006488	dolichol-linked oligosaccharide biosynthetic process	5	3.78E-3
GO:0022604	regulation of cell morphogenesis	45	3.89E-3
GO:1902680	positive regulation of RNA biosynthetic process	110	4.05E-3
GO:0051241	negative regulation of multicellular organismal process	79	4.16E-3
GO:1902591	single-organism membrane budding	6	4.24E-3
GO:1903426	regulation of reactive oxygen species biosynthetic process	12	4.36E-3
GO:0035239	tube morphogenesis	40	4.36E-3
GO:0045937	positive regulation of phosphate metabolic process	76	4.36E-3
GO:0006090	pyruvate metabolic process	11	4.45E-3
GO:0048858	cell projection morphogenesis	53	4.45E-3
GO:0010557	positive regulation of macromolecule biosynthetic process	120	4.48E-3
GO:0051961	negative regulation of nervous system development	28	4.48E-3
GO:2000147	positive regulation of cell motility	36	4.58E-3
GO:0072001	renal system development	32	4.58E-3
GO:0031329	regulation of cellular catabolic process	54	4.63E-3
GO:0070374	positive regulation of ERK1 and ERK2 cascade	19	4.95E-3
GO:1901215	negative regulation of neuron death	22	4.96E-3
GO:0044085	cellular component biogenesis	129	4.96E-3
GO:0070887	cellular response to chemical stimulus	125	5.04E-3
GO:0045859	regulation of protein kinase activity	56	5.04E-3
GO:0051336	regulation of hydrolase activity	88	5.13E-3
GO:0051783	regulation of nuclear division	20	5.31E-3
GO:0010975	regulation of neuron projection development	36	5.39E-3
GO:0019219	regulation of nucleobase-containing compound metabolic process	219	5.57E-3
GO:0072384	organelle transport along microtubule	8	5.58E-3
GO:1901214	regulation of neuron death	28	5.87E-3
GO:0051099	positive regulation of binding	17	5.89E-3
GO:0035725	sodium ion transmembrane transport	17	5.89E-3
GO:0006333	chromatin assembly or disassembly	16	6.4E-3

GO:0032400	melanosome localization	7	6.4E-3
GO:0051668	localization within membrane	7	6.4E-3
GO:0048534	hematopoietic or lymphoid organ development	56	6.4E-3
GO:0051248	negative regulation of protein metabolic process	77	6.4E-3
GO:0002682	regulation of immune system process	83	6.75E-3
GO:0098602	single organism cell adhesion	44	6.89E-3
GO:0009101	glycoprotein biosynthetic process	29	6.91E-3
GO:0032787	monocarboxylic acid metabolic process	41	7,00E-03
GO:0071310	cellular response to organic substance	103	7.08E-3
GO:0007346	regulation of mitotic cell cycle	40	7.1E-3
GO:0080135	regulation of cellular response to stress	57	7.12E-3
GO:0010769	regulation of cell morphogenesis involved in differentiation	31	7.2E-3
GO:0065003	macromolecular complex assembly	81	7.21E-3
GO:0047497	mitochondrion transport along microtubule	4	7.25E-3
GO:0051173	positive regulation of nitrogen compound metabolic process	127	7.39E-3
GO:0051254	positive regulation of RNA metabolic process	111	7.53E-3
GO:1903532	positive regulation of secretion by cell	32	7.7E-3
GO:0006508	proteolysis	78	7.96E-3
GO:0061138	morphogenesis of a branching epithelium	24	8.04E-3
GO:0016568	chromatin modification	45	8.29E-3
GO:0032990	cell part morphogenesis	54	8.33E-3
GO:0051875	pigment granule localization	7	8.34E-3
GO:0045428	regulation of nitric oxide biosynthetic process	10	8.58E-3
GO:0051057	positive regulation of small GTPase mediated signal transduction	8	8.81E-3
GO:0090342	regulation of cell aging	8	8.81E-3
GO:0010629	negative regulation of gene expression	105	9.17E-3
GO:0010628	positive regulation of gene expression	123	9.32E-3
GO:1903530	regulation of secretion by cell	51	9.84E-3
GO:0018108	peptidyl-tyrosine phosphorylation	21	9.9E-3
GO:0043523	regulation of neuron apoptotic process	24	9.99E-3
GO:0040017	positive regulation of locomotion	36	1.01E-2
GO:0018210	peptidyl-threonine modification	10	1.02E-2
GO:0051240	positive regulation of multicellular organismal process	102	1.03E-2
GO:0050679	positive regulation of epithelial cell proliferation	20	1.04E-2
GO:0048754	branching morphogenesis of an epithelial tube	21	1.07E-2
GO:0009100	glycoprotein metabolic process	31	1.07E-2
GO:0030029	actin filament-based process	38	1.07E-2
GO:0009628	response to abiotic stimulus	75	1.08E-2
GO:0044271	cellular nitrogen compound biosynthetic process	189	1.09E-2
GO:0030155	regulation of cell adhesion	50	1.09E-2
GO:0051338	regulation of transferase activity	62	1.11E-2
GO:1901575	organic substance catabolic process	90	1.11E-2
GO:0010256	endomembrane system organization	37	1.14E-2
GO:0018212	peptidyl-tyrosine modification	21	1.14E-2
GO:0016337	single organismal cell-cell adhesion	41	1.14E-2
GO:0043524	negative regulation of neuron apoptotic process	19	1.17E-2

GO:0072012	glomerulus vasculature development	6	1.18E-2
GO:0060612	adipose tissue development	9	1.18E-2
GO:0014070	response to organic cyclic compound	65	1.24E-2
GO:0001525	angiogenesis	32	1.26E-2
GO:0030036	actin cytoskeleton organization	36	1.27E-2
GO:2001233	regulation of apoptotic signaling pathway	38	1.36E-2
GO:0006814	sodium ion transport	20	1.43E-2
GO:0030163	protein catabolic process	44	1.43E-2
GO:0032413	negative regulation of ion transmembrane transporter activity	9	1.43E-2
GO:0038083	peptidyl-tyrosine autophosphorylation	9	1.43E-2
GO:0051259	protein oligomerization	37	1.45E-2
GO:0030888	regulation of B cell proliferation	11	1.48E-2
GO:0001822	kidney development	29	1.48E-2
GO:0060537	muscle tissue development	32	1.48E-2
GO:0055085	transmembrane transport	74	1.48E-2
GO:0030111	regulation of Wnt signaling pathway	26	1.48E-2
GO:0009891	positive regulation of biosynthetic process	126	1.49E-2
GO:0051093	negative regulation of developmental process	69	1.51E-2
GO:0043393	regulation of protein binding	20	1.52E-2
GO:0031328	positive regulation of cellular biosynthetic process	124	1.53E-2
GO:0002520	immune system development	56	1.56E-2
GO:0007568	aging	26	1.57E-2
GO:1901360	organic cyclic compound metabolic process	257	1.58E-2
GO:0045429	positive regulation of nitric oxide biosynthetic process	8	1.62E-2
GO:0070647	protein modification by small protein conjugation or removal	57	1.65E-2
GO:0044257	cellular protein catabolic process	41	1.69E-2
GO:0006725	cellular aromatic compound metabolic process	245	1.75E-2
GO:0044712	single-organism catabolic process	57	1.92E-2
GO:0048646	anatomical structure formation involved in morphogenesis	79	2,00E-02
GO:0003008	system process	92	2,00E-02
GO:0031327	negative regulation of cellular biosynthetic process	100	2.01E-2
GO:0032269	negative regulation of cellular protein metabolic process	70	2.02E-2
GO:0048514	blood vessel morphogenesis	38	2.05E-2
GO:0002009	morphogenesis of an epithelium	44	2.05E-2
GO:0048489	synaptic vesicle transport	15	2.06E-2
GO:0097480	establishment of synaptic vesicle localization	15	2.06E-2
GO:0051174	regulation of phosphorus metabolic process	107	2.08E-2
GO:0061440	kidney vasculature development	6	2.11E-2
GO:0061437	renal system vasculature development	6	2.11E-2
GO:0043436	oxoacid metabolic process	62	2.11E-2
GO:0048732	gland development	40	2.17E-2
GO:0048709	oligodendrocyte differentiation	11	2.17E-2
GO:0006325	chromatin organization	47	2.18E-2
GO:0001654	eye development	35	2.18E-2
GO:0019752	carboxylic acid metabolic process	58	2.2E-2
GO:0050865	regulation of cell activation	39	2.23E-2

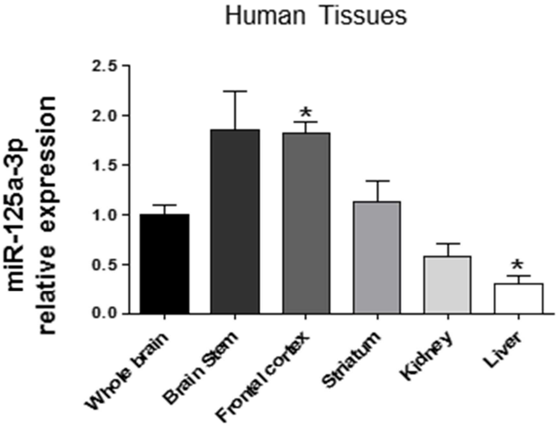
GO:0009890	negative regulation of biosynthetic process	101	2.25E-2
GO:0002768	immune response-regulating cell surface receptor signaling pathway	14	2.25E-2
GO:0030217	T cell differentiation	18	2.35E-2
GO:0051347	positive regulation of transferase activity	41	2.36E-2
GO:0014706	striated muscle tissue development	30	2.37E-2
GO:0051260	protein homooligomerization	26	2.37E-2
GO:0097479	synaptic vesicle localization	15	2.45E-2
GO:0046887	positive regulation of hormone secretion	15	2.45E-2
GO:0019220	regulation of phosphate metabolic process	106	2.56E-2
GO:0032446	protein modification by small protein conjugation	49	2.58E-2
GO:0002064	epithelial cell development	24	2.59E-2
GO:0006139	nucleobase-containing compound metabolic process	234	2.59E-2
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	118	2.62E-2
GO:0009057	macromolecule catabolic process	55	2.62E-2
GO:0060740	prostate gland epithelium morphogenesis	7	2.64E-2
GO:0043549	regulation of kinase activity	56	2.66E-2
GO:0046483	heterocycle metabolic process	242	2.67E-2
GO:1903053	regulation of extracellular matrix organization	6	2.69E-2
GO:0031497	chromatin assembly	13	2.71E-2
GO:0009605	response to external stimulus	112	2.72E-2
GO:0043065	positive regulation of apoptotic process	45	2.72E-2
GO:0045892	negative regulation of transcription, DNA-templated	84	2.74E-2
GO:0045860	positive regulation of protein kinase activity	36	2.74E-2
GO:0008104	protein localization	108	2.79E-2
GO:0045597	positive regulation of cell differentiation	66	2.8E-2
GO:0007411	axon guidance	20	2.87E-2
GO:0044265	cellular macromolecule catabolic process	50	2.89E-2
GO:0002764	immune response-regulating signaling pathway	18	2.89E-2
GO:0072073	kidney epithelium development	18	2.89E-2
GO:0051223	regulation of protein transport	56	2.89E-2
GO:0051603	proteolysis involved in cellular protein catabolic process	39	2.92E-2
GO:0002521	leukocyte differentiation	31	2.93E-2
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	95	2.94E-2
GO:0009896	positive regulation of catabolic process	36	2.96E-2
GO:0045725	positive regulation of glycogen biosynthetic process	5	2.96E-2
GO:0022612	gland morphogenesis	16	2.99E-2
GO:0034109	homotypic cell-cell adhesion	29	3,00E-02
GO:0006900	membrane budding	9	3.02E-2
GO:0097485	neuron projection guidance	20	3.02E-2
GO:0044092	negative regulation of molecular function	73	3.02E-2
GO:0045930	negative regulation of mitotic cell cycle	19	3.06E-2
GO:0048857	neural nucleus development	10	3.09E-2
GO:0060512	prostate gland morphogenesis	7	3.13E-2
GO:0060627	regulation of vesicle-mediated transport	35	3.16E-2
GO:0006807	nitrogen compound metabolic process	279	3.18E-2
GO:0043068	positive regulation of programmed cell death	45	3.2E-2

GO:0051253	negative regulation of RNA metabolic process	88	3.25E-2
GO:0043087	regulation of GTPase activity	42	3.25E-2
GO:0032733	positive regulation of interleukin-10 production	6	3.33E-2
GO:0034220	ion transmembrane transport	59	3.33E-2
GO:0045184	establishment of protein localization	83	3.36E-2
GO:0007088	regulation of mitotic nuclear division	15	3.36E-2
GO:0006082	organic acid metabolic process	62	3.38E-2
GO:0007519	skeletal muscle tissue development	17	3.54E-2
GO:0007159	leukocyte cell-cell adhesion	27	3.54E-2
GO:0008285	negative regulation of cell proliferation	49	3.65E-2
GO:0001504	neurotransmitter uptake	4	3.68E-2
GO:0051654	establishment of mitochondrion localization	4	3.68E-2
GO:0050851	antigen receptor-mediated signaling pathway	11	3.79E-2
GO:0030001	metal ion transport	46	3.79E-2
GO:1903507	negative regulation of nucleic acid-templated transcription	84	3.88E-2
GO:1902679	negative regulation of RNA biosynthetic process	85	3.94E-2
GO:0006091	generation of precursor metabolites and energy	23	3.94E-2
GO:0030238	male sex determination	5	3.94E-2
GO:0070875	positive regulation of glycogen metabolic process	5	3.94E-2
GO:1901881	positive regulation of protein depolymerization	5	3.94E-2
GO:0044708	single-organism behavior	38	3.94E-2
GO:0032479	regulation of type I interferon production	9	3.94E-2
GO:0009185	ribonucleoside diphosphate metabolic process	9	3.94E-2
GO:0044087	regulation of cellular component biogenesis	53	3.97E-2
GO:0043010	camera-type eye development	31	3.98E-2
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	91	4.02E-2
GO:0050770	regulation of axonogenesis	16	4.02E-2
GO:0051172	negative regulation of nitrogen compound metabolic process	100	4.02E-2
GO:2000772	regulation of cellular senescence	6	4.1E-2
GO:2000826	regulation of heart morphogenesis	6	4.1E-2
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	11	4.16E-2
GO:0044281	small molecule metabolic process	98	4.22E-2
GO:0002429	immune response-activating cell surface receptor signaling pathway	12	4.25E-2
GO:1903428	positive regulation of reactive oxygen species biosynthetic process	8	4.3E-2
GO:0006836	neurotransmitter transport	16	4.33E-2
GO:0016567	protein ubiquitination	45	4.33E-2
GO:0032410	negative regulation of transporter activity	9	4.48E-2
GO:0090304	nucleic acid metabolic process	208	4.5E-2
GO:0070201	regulation of establishment of protein localization	58	4.52E-2
GO:0033674	positive regulation of kinase activity	37	4.57E-2
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	25	4.59E-2
GO:0010634	positive regulation of epithelial cell migration	13	4.6E-2
GO:0001959	regulation of cytokine-mediated signaling pathway	11	4.6E-2
GO:0009132	nucleoside diphosphate metabolic process	11	4.6E-2
GO:0015711	organic anion transport	28	4.62E-2
GO:0030178	negative regulation of Wnt signaling pathway	16	4.64E-2

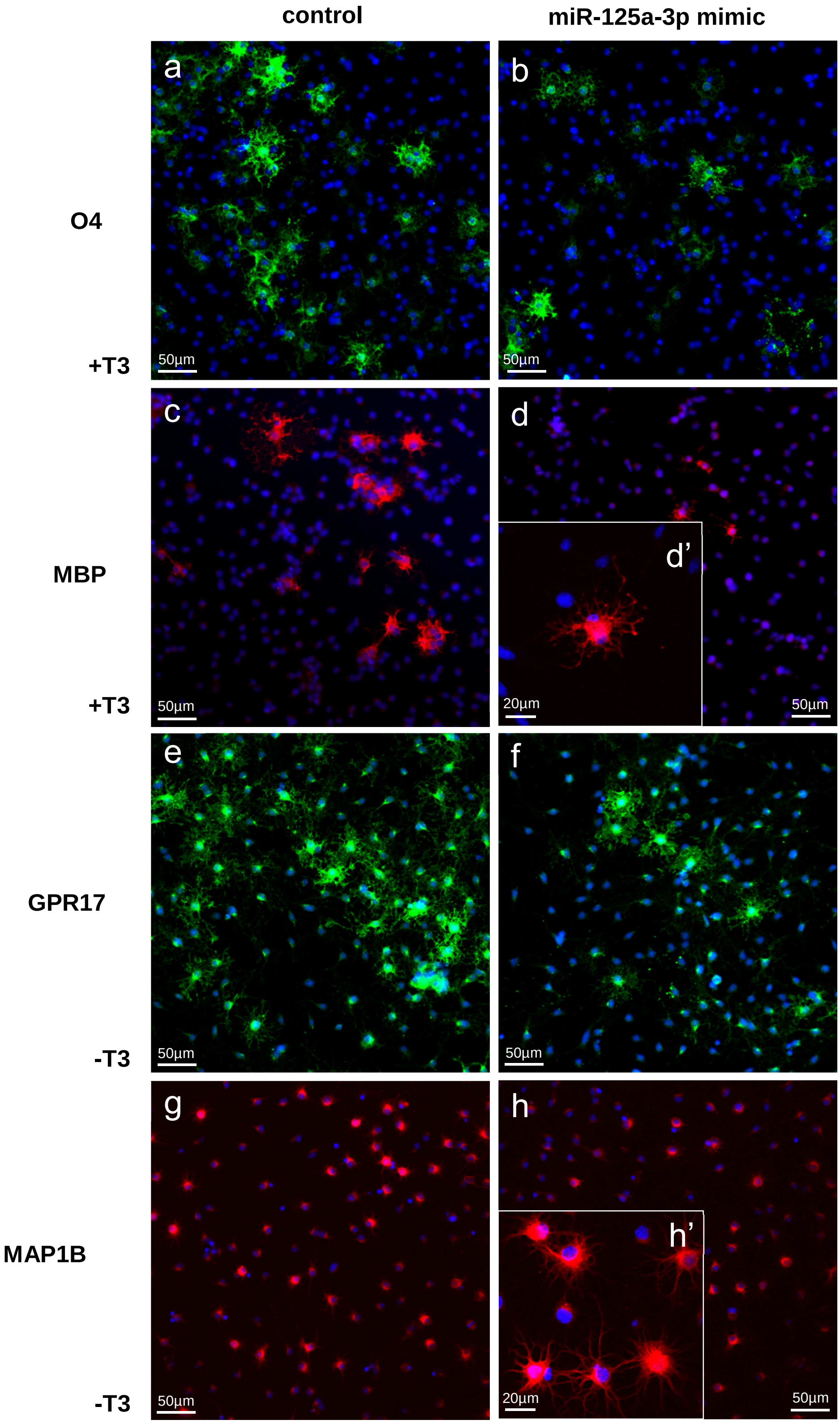
GO:0044255	cellular lipid metabolic process	55	4.66E-2
GO:0010942	positive regulation of cell death	46	4.9E-2
GO:0016070	RNA metabolic process	184	4.94E-2
GO:0033059	cellular pigmentation	8	4.96E-2

Supplementary Table S2. List of molecular interactions leading miR-125a-3p to inhibit MBP expression.

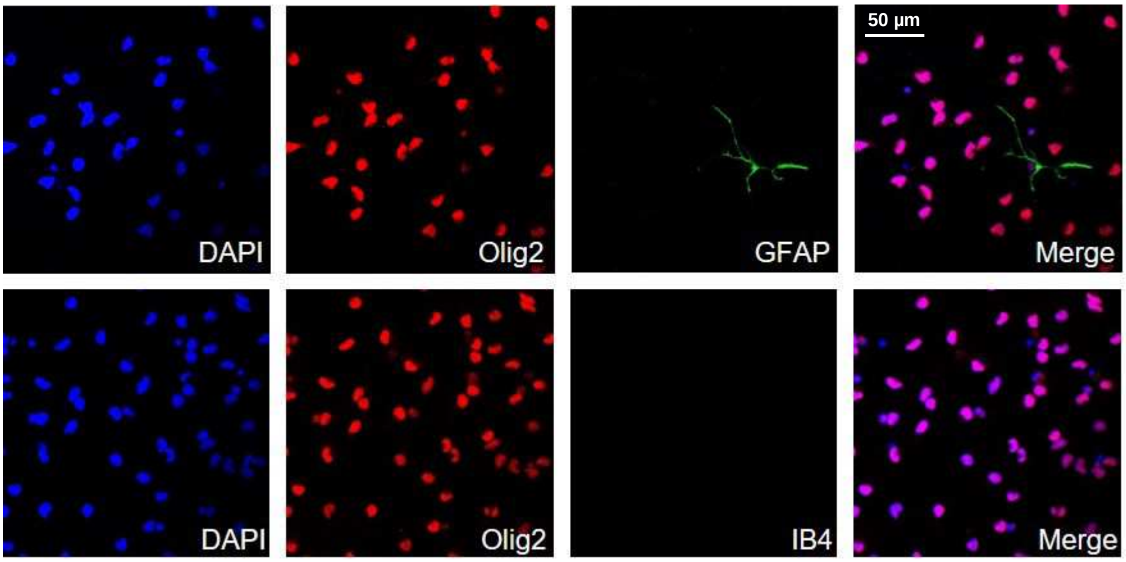
Molecule A	**Molecule B**	**Type of interaction**	**Function**	**Reference**
miR-125a-3p	FYN	Binding	Inhibition of Fyn expression	Ninio-Many et al., 2013
miR-125a-3p	SMAD4	Binding	Inhibition of Smad4 expression	Boissart et al., 2012
miR-125a-3p	RHOA	Binding	Inhibition of RhoA expression	Huang et al., 2013
miR-125a-3p	P38	Binding	Inhibition of p38 expression	Dong et al., 2014
miR-125a-3p	NRG-1	Binding	Inhibition of NRG-1 expression	Yin et al., 2015
FYN	QKI	Phosphorylation	Activation of QKI	Lu et al., 2005
FYN	MBP	Indirect mechanism	Stimulation of MBP promoter	Umemori et al., 1999
FYN	RHOA	Phosphorylation	Inhibition of RHOA via p190RhoGAP activation	Wolf t al., 2001; Liang et al., 2004
QKI	MAP1B	Binding	Stabilization of MAP1B mRNA	Zhao et al., 2006
QKI	MBP	Binding	Stabilization of MBP mRNA	Li et al., 2000
NRG-1	MBP	Indirect mechanism	Promotion of MBP expression	Cannella et al., 1998
NRG-1	FYN	Indirect mechanism	Binding of NRG-1 to ErbB4 increases Fyn activation	Bjarnadottir et al., 2007
RHOA	P38	Indirect mechanism	Promotion of p38 activation	Ivaska et al., 1999
SMAD4	P38	Indirect mechanism	Activation of P38 via MAPKKK	Takekawa et al., 2008
P38	MBP	Phosphorylation	Promotes compaction of myelin	Unpublished observation



Supplementary Figure S1. miR-125a-3p relative expression was analyzed using Taqman assay in different human tissues and compared to level measured in whole brain. Neural tissues showed higher expression with respect to other tissues. Data were expressed as mean ± SEM, n = 3; two-tailed unpaired t test *p < 0.05 vs. whole brain.



Supplementary Figure S2. Representative micrographs of OPC cultures 48h after transfection with miR-125a-3p mimic compared to control cultures, at both low (a-h) and high magnification (d’, h’). After culturing in a standard proliferation medium, OPCs were transfected and differentiated either in the presence (a-d) or in the absence (e-h) of the T3 hormone, according to a “fast” and a “slow differentiation protocol”, respectively. Then, cells were fixed and stained for the selected markers: (a,b) O4, (c,d,d’) MBP, (e,f) GPR17, (g,h,h’) MAP1B.



Supplementary Figure S3. Representative images of OPC cultures to investigate the potential contamination by other cell types. After culturing in a standard proliferation medium, OPCs were differentiated for 48 hours in the presence of the T3 hormone. Then, cells were fixed and stained for the selected markers: Olig2 for oligodendrocytes, GFAP for astrocytes and Ib4 for microglia cells.